

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/574,306
Source: IFWP
Date Processed by STIC: 03/13/2007

ENTERED



IFWP

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DATE: 03/13/2007

PATENT APPLICATION: US/10/574,306

TIME: 08:29:13

Input Set : A:\50458.002001.txt

Output Set: N:\CRF4\03132007\J574306.raw

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3 <110> APPLICANT: Korherr, Christian
5 <120> TITLE OF INVENTION: Medical Use of TBK-1 or of Inhibitors Thereof
7 <130> FILE REFERENCE: 50458/002001
9 <140> CURRENT APPLICATION NUMBER: US 10/574,306
10 <141> CURRENT FILING DATE: 2006-04-03
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010996
13 <151> PRIOR FILING DATE: 2004-10-01
15 <150> PRIOR APPLICATION NUMBER: US 60/508,100
16 <151> PRIOR FILING DATE: 2003-10-02
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3031
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 taacaagagg attgcctgat ccagccaaga tgcagagcac ttctaatacat ctgtggcttt      120
32 tatctgatat tttaggccaa ggagctactg caaatgtctt tcgtggaaga cataagaaaa      180
34 ctggtgattt atttgctatc aaagtattta ataacataag cttccttcgt ccagtggatg      240
36 ttcaaagtga agaatttgaa gtgttgaaaa aactcaatca caaaaatatt gtcaaattat      300
38 ttgctattga agaggagaca acaacaagac ataaagtact tattatggaa ttttgtccat      360
40 gtgggagttt atacactgtt ttagaagaac cttctaattgc ctatggacta ccagaatctg      420
42 aattcttaat tgttttgcca gatgtggtgg gtggaatgaa tcatctacga gagaatggta      480
44 tagtgcaccg tgatatcaag ccaggaaata tcatgctgtg tataggggaa gatggacagt      540
46 ctgtgtacaa actcacagat tttggtgcag ctagagaatt agaagatgat gagcagtttg      600
48 tttctctgta tggcacagaa gaatatattgc accctgatat gtatgagaga gcagtgctaa      660
50 gaaaagatca tcagaagaaa tatggagcaa cagttgatct ttggagcatt ggggtaacat      720
52 tttaccatgc agctactgga tcaactgccat ttagaccctt tgaagggcct cgtaggaata      780
54 aagaagtgat gtataaaata attacaggaa agccttcttg tgcaatatct ggagtacaga      840
56 aagcagaaaa tggaccaatt gactggagtg gagacatgcc tgtttcttgc agtctttctc      900
58 ggggtcttca ggttctactt acccctgttc ttgcaaacat ccttgaagca gatcaggaaa      960
60 agtgttgggg ttttgaccag tttttgacag aaactagtga tatacttcac cgaatggtaa      1020
62 ttcattgttt ttcgctacaa caaatgacag ctcataagat ttatattcat agctataata      1080
64 ctgctactat atttcatgaa ctggtatata aacaaaccaa aattatttct tcaaatacaag      1140
66 aacttatcta cgaagggcga cgcttagtct tagaacctgg aaggctggca caacatttcc      1200
68 ctaaaactac tgaggaaaac cctatatattg tagtaagccg ggaacctctg aataccatag      1260
70 gattaatata tgaaaaaatt tccctcccta aagtacatcc acgttatgat ttagacgggg      1320
72 atgctagcat ggctaaggca ataacagggg ttgtgtgtta tgacctgaga attgccagta      1380
74 ccttactgct ttatcaggaa ttaatgcgaa aggggatacg atggctgatt gaattaatta      1440
76 aagatgatta caatgaaact gttcacaaaa agacagaagt tgtgatcaca ttggatttct      1500
78 gtatcagaaa cattgaaaaa actgtgaaag tatatgaaaa gttgatgaag atcaacctgg      1560
80 aagcggcaga gttaggtgaa atttcagaca tacacaccaa attggtgaga ctttccagtt      1620

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82 ctcaggaac aatagaaacc agtcttcagg atatcgacag cagattatct ccaggtggat 1680
84 cactggcaga cgcattgggca catcaagaag gcactcatcc gaaagacaga aatgtagaaa 1740
86 aactacaagt cctgttaaat tgcattgacag agattttacta tcagttcaaa aaagacaaaag 1800
88 cagaacgtag attagcttat aatgaagaac aaatccacaa atttgataag caaaaactgt 1860
90 attaccatgc cacaaaagct atgacgcact ttacagatga atgtgttaaa aagtatgagg 1920
92 catttttgaa taagtcagaa gaatggataa gaaagatgct tcatcttagg aaacagttat 1980
94 tatcgctgac taatcagtgt tttgatattg aagaagaagt atcaaaatat caagaatata 2040
96 ctaatgagtt acaagaaact ctgcctcaga aaatgtttac agcttccagt ggaatcaaac 2100
98 ataccatgac cccaatttat ccaagttcta acacattagt agaaatgact cttggtatga 2160
100 agaaattaaa ggaagagatg gaaggggtgg ttaaagaact tgctgaaaat aaccacattt 2220
102 tagaaagggt tggctcttta accatggatg gtggccttcg caacgttgac tgtcttttagc 2280
104 tttctaatag aagtttaaga aaagtttccg ttgcacaaag aaaataacgc ttgggcatta 2340
106 aatgaatgcc tttatagata gtcacttggt tctacaattc agtatttgat gtggtcgtgt 2400
108 aaatatgtac aatatgttaa atacataaaa aatatacaaa tttttggctg ctgtgaagat 2460
110 gtaattttat cttttaacat ttataattat atgaggaaat ttgacctcag tgatcacgag 2520
112 aagaaagcca tgaccgacca atatgttgac atactgatcc tctactctga gtggggctaa 2580
114 ataagttatt ttctctgacc gcctactgga aatattttta agtggaaacca aaataggcat 2640
116 ccttacaat caggaagact gacttgacac gtttgtaaat ggtagaacgg tggctactgt 2700
118 gagtggggag cagaaccgca ccactgttat actgggataa caattttttt gagaaggata 2760
120 aagtggcatt attttatttt acaaggtgcc cagatcccag ttatccttgt atccatgtaa 2820
122 tttcagatga attattaagc aaacatttta aagtgaattc attattaaaa actattcatt 2880
124 tttttccttt ggccataaat gtgtaattgt cattaaaatt ctáaggatcat ttcaactgtt 2940
126 ttaagctgta tatttcttta attctgctta ctatttcatg gaaaaaaata aattttctca 3000
128 ttttaatgta aagaaaaaaa aaaaaaaaaa a 3031

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131 <210> SEQ ID NO: 2

132 <211> LENGTH: 729

133 <212> TYPE: PRT

134 <213> ORGANISM: Homo sapiens

136 <400> SEQUENCE: 2

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138 Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
139 1 5 10 15
142 Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
143 20 25 30
146 Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
147 35 40 45
150 Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
151 50 55 60
154 Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Thr Thr Arg
155 65 70 75 80
158 His Lys Val Leu Ile Met Glu Phe Cys Pro Cys Gly Ser Leu Tyr Thr
159 85 90 95
162 Val Leu Glu Glu Pro Ser Asn Ala Tyr Gly Leu Pro Glu Ser Glu Phe
163 100 105 110
166 Leu Ile Val Leu Arg Asp Val Val Gly Gly Met Asn His Leu Arg Glu
167 115 120 125
170 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Val
171 130 135 140
174 Ile Gly Glu Asp Gly Gln Ser Val Tyr Lys Leu Thr Asp Phe Gly Ala
175 145 150 155 160

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178 Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val Ser Leu Tyr Gly Thr
179              165              170              175
182 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
183              180              185              190
186 Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp Leu Trp Ser Ile Gly
187              195              200              205
190 Val Thr Phe Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Arg Pro Phe
191              210              215              220
194 Glu Gly Pro Arg Arg Asn Lys Glu Val Met Tyr Lys Ile Ile Thr Gly
195 225              230              235              240
198 Lys Pro Ser Gly Ala Ile Ser Gly Val Gln Lys Ala Glu Asn Gly Pro
199              245              250              255
202 Ile Asp Trp Ser Gly Asp Met Pro Val Ser Cys Ser Leu Ser Arg Gly
203              260              265              270
206 Leu Gln Val Leu Leu Thr Pro Val Leu Ala Asn Ile Leu Glu Ala Asp
207              275              280              285
210 Gln Glu Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp
211              290              295              300
214 Ile Leu His Arg Met Val Ile His Val Phe Ser Leu Gln Gln Met Thr
215 305              310              315              320
218 Ala His Lys Ile Tyr Ile His Ser Tyr Asn Thr Ala Thr Ile Phe His
219              325              330              335
222 Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln Glu Leu
223              340              345              350
226 Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu Ala Gln
227              355              360              365
230 His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val Ser Arg
231              370              375              380
234 Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser Leu Pro
235 385              390              395              400
238 Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met Ala Lys
239              405              410              415
242 Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser Thr Leu
243              420              425              430
246 Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu Ile Glu
247              435              440              445
250 Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr Glu Val
251              450              455              460
254 Val Ile Thr Leu Asp Phe Cys Ile Arg Asn Ile Glu Lys Thr Val Lys
255 465              470              475              480
258 Val Tyr Glu Lys Leu Met Lys Ile Asn Leu Glu Ala Ala Glu Leu Gly
259              485              490              495
262 Glu Ile Ser Asp Ile His Thr Lys Leu Leu Arg Leu Ser Ser Ser Gln
263              500              505              510
266 Gly Thr Ile Glu Thr Ser Leu Gln Asp Ile Asp Ser Arg Leu Ser Pro
267              515              520              525
270 Gly Gly Ser Leu Ala Asp Ala Trp Ala His Gln Glu Gly Thr His Pro
271              530              535              540
274 Lys Asp Arg Asn Val Glu Lys Leu Gln Val Leu Leu Asn Cys Met Thr

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275 545          550          555          560
278 Glu Ile Tyr Tyr Gln Phe Lys Lys Asp Lys Ala Glu Arg Arg Leu Ala
279          565          570          575
282 Tyr Asn Glu Glu Gln Ile His Lys Phe Asp Lys Gln Lys Leu Tyr Tyr
283          580          585          590
286 His Ala Thr Lys Ala Met Thr His Phe Thr Asp Glu Cys Val Lys Lys
287          595          600          605
290 Tyr Glu Ala Phe Leu Asn Lys Ser Glu Glu Trp Ile Arg Lys Met Leu
291          610          615          620
294 His Leu Arg Lys Gln Leu Leu Ser Leu Thr Asn Gln Cys Phe Asp Ile
295 625          630          635          640
298 Glu Glu Glu Val Ser Lys Tyr Gln Glu Tyr Thr Asn Glu Leu Gln Glu
299          645          650          655
302 Thr Leu Pro Gln Lys Met Phe Thr Ala Ser Ser Gly Ile Lys His Thr
303          660          665          670
306 Met Thr Pro Ile Tyr Pro Ser Ser Asn Thr Leu Val Glu Met Thr Leu
307          675          680          685
310 Gly Met Lys Lys Leu Lys Glu Glu Met Glu Gly Val Val Lys Glu Leu
311          690          695          700
314 Ala Glu Asn Asn His Ile Leu Glu Arg Phe Gly Ser Leu Thr Met Asp
315 705          710          715          720
318 Gly Gly Leu Arg Asn Val Asp Cys Leu
319          725

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322 <210> SEQ ID NO: 3

323 <211> LENGTH: 19

324 <212> TYPE: RNA

325 <213> ORGANISM: artificial

327 <220> FEATURE:

328 <223> OTHER INFORMATION: oligonucleotide siTBK-1 sense

330 <400> SEQUENCE: 3

331 ggagacaaca acaagacau

19

334 <210> SEQ ID NO: 4

335 <211> LENGTH: 20

336 <212> TYPE: RNA

337 <213> ORGANISM: artificial

339 <220> FEATURE:

340 <223> OTHER INFORMATION: oligonucleotide siTBK-1 antisense

342 <400> SEQUENCE: 4

343 augucuuguu guugucuccc

20

346 <210> SEQ ID NO: 5

347 <211> LENGTH: 23

348 <212> TYPE: DNA

349 <213> ORGANISM: artificial

351 <220> FEATURE:

352 <223> OTHER INFORMATION: oligonucleotide TBK-1 sense

354 <400> SEQUENCE: 5

355 ttgaagagga gacaacaaca aga

23

358 <210> SEQ ID NO: 6

359 <211> LENGTH: 19

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360 <212> TYPE: DNA
361 <213> ORGANISM: artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: oligonucleotide TBK-1 antisense
366 <400> SEQUENCE: 6
367 cattccaccc accacatct 19
370 <210> SEQ ID NO: 7
371 <211> LENGTH: 20
372 <212> TYPE: DNA
373 <213> ORGANISM: artificial
375 <220> FEATURE:
376 <223> OTHER INFORMATION: oligonucleotide VEGF sense
378 <400> SEQUENCE: 7
379 cttgccttgc tgctctacct 20
382 <210> SEQ ID NO: 8
383 <211> LENGTH: 20
384 <212> TYPE: DNA
385 <213> ORGANISM: artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: oligonucleotide VEGF antisense
390 <400> SEQUENCE: 8
391 gattctgccc tctctcttct 20
394 <210> SEQ ID NO: 9
395 <211> LENGTH: 20
396 <212> TYPE: DNA
397 <213> ORGANISM: artificial
399 <220> FEATURE:
400 <223> OTHER INFORMATION: oligonucleotide Rantes sense
402 <400> SEQUENCE: 9
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406 <210> SEQ ID NO: 10
407 <211> LENGTH: 20
408 <212> TYPE: DNA
409 <213> ORGANISM: artificial
411 <220> FEATURE:
412 <223> OTHER INFORMATION: oligonucleotide Rantes antisense
414 <400> SEQUENCE: 10
415 gcacttgcca ctggtgtaga 20

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RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY

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